

SEQUENCE LISTING

<110> FUCHS, Sara
 BARCHAN, Dora
 SOUROUJON, Miriam

<120> RECOMBINANT FRAGMENTS OF THE HUMAN ACETYLCHOLINE RECEPTOR AND THEIR USE FOR TREATMENT OF MYASTHENIA GRAVIS

<130> FUCHS=2A

<140> NOT YET ASSIGNED

<141> 2001-03-29

<150> 09/423,398

<151> 1999-11-08

<150> PCT/IL98/00211

<151> 1998-05-06

<160> 32

<170> PatentIn version 3.0

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<211> 630

<212> DNA

<213> Homo sapiens

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atcaatgtgg atgaagtaaa tcagatcgtg acaaccaatg tgcgtctgaa acagcaatgg 180

gtggattaca acctaaaatg gaatccagat gactatggcg gtgtgaaaaa aattcacatt 240

ccttcagaaa agatctggcg cccagacott gttctctata acgatgcaga tgggtgacttt 300

gctattgtca agttcaccaa agtgetcctg cagtacactg gccacatcac gtggacacct 360

ccagccatct ttaaaagcta ctgtgagatc atcgtcacc acccttccctt tgatgaacag 420

aactgcagca tgaagctggg cacctggacc tacgacggct ctgtcgtggc catcaaccgc 480

gaaagcgacc agccagacct gagcaacttc atggagagcg gggagtgggt gatcaaggag 540

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Ala Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp Glu Val Asn Gln
    35                      40                      45

Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gln Trp Val Asp Tyr Asn
    50                      55                      60

Leu Lys Trp Asn Pro Asp Asp Tyr Gly Gly Val Lys Lys Ile His Ile
    65                      70                      75                      80

Pro Ser Glu Lys Ile Trp Arg Pro Asp Leu Val Leu Tyr Asn Asn Ala
    85                      90                      95

Asp Gly Asp Phe Ala Ile Val Lys Phe Thr Lys Val Leu Leu Gln Tyr
    100                     105                     110

Thr Gly His Ile Thr Trp Thr Pro Pro Ala Ile Phe Lys Ser Tyr Cys
    115                     120                     125

Glu Ile Ile Val Thr His Phe Pro Phe Asp Glu Gln Asn Cys Ser Met
    130                     135                     140

Lys Leu Gly Thr Trp Thr Tyr Asp Gly Ser Val Val Ala Ile Asn Pro
    145                     150                     155                     160

Glu Ser Asp Gln Pro Asp Leu Ser Asn Phe Met Glu Ser Gly Glu Trp
    165                     170                     175

Val Ile Lys Glu Ser Arg Gly Trp Lys His Ser Val Thr Tyr Ser Cys
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Cys Pro Asp Thr Pro Tyr Leu Asp Ile Thr Tyr His Phe Val Met Gln
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Arg Leu
    210

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catctgcagg atgag 75

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 gcagatggtg actttgctat tgtcaagttc accaaagtgc tcttgacagta cactggccac 420
 atcacgtgga cacctccagc catctttaaa agctactgtg agatcatcgt caccactttt 480
 ccttttgatg aacagaactg cagcatgaag ctgggcacct ggacctacga cggctctgtc 540
 gtggccatca acccggaag cgaccagcca gacctgagca acttcatgga gagcggggag 600
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 20 25 30
 Ala Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp Glu Val Asn Gln
 35 40 45
 Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gly Asp Met Val Asp Leu
 50 55 60
 Pro Arg Pro Ser Cys Val Thr Leu Gly Val Pro Leu Phe Ser His Leu
 65 70 75 80
 Gln Asp Glu Gln Trp Val Asp Tyr Asn Leu Lys Trp Asn Pro Asp Asp
 85 90 95
 Tyr Gly Gly Val Lys Lys Ile His Ile Pro Ser Glu Lys Ile Trp Arg
 100 105 110
 Pro Asp Leu Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe Ala Ile Val
 115 120 125
 Lys Phe Thr Lys Val Leu Leu Gln Tyr Thr Gly His Ile Thr Trp Thr

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130          135          140
Pro Pro Ala Ile Phe Lys Ser Tyr Cys Glu Ile Ile Val Thr His Phe
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Pro Phe Asp Glu Gln Asn Cys Ser Met Lys Leu Gly Thr Trp Thr Tyr
165          170          175
Asp Gly Ser Val Val Ala Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu
180          185          190
Ser Asn Phe Met Glu Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly
195          200          205
Trp Lys His Ser Val Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu
210          215          220
Asp Ile Thr Tyr His Phe Val Met Gln Arg Leu
225          230          235

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atcaatgttg atgaagtaaa tcagatcgtg acaaccaatg tgcgtctgaa acaggggtgac      180
atggtagatc tgccacgccc cagctgcgtg actttgggag ttctttgtt ttctcatctg      240
caggatgagc aatgggtgga ttacaacctt aaatggaatc cagatgacta tggcgggtgtg      300
aaaaaaattc acattccttc agaaaagatc tggcgcccag accttggttct ctataacgat      360
gcagatggtg actttgctat tgtcaagttc accaaagtgc tctgcagta cactggccac      420
atcacgtgga cacctccagc catctttaaa agctactgtg agatcatcgt caccactttt      480
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gtggccatca acccgaaaag cgaccagcca gacctgagca acttcatgga gagcggggag      600
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<212> PRT
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Ser Val Val Arg Pro Val Glu Asp His Arg Gln Val Val Glu Val Thr
20          25          30

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Ala Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp Glu Val Asn Gln
      35                      40                      45

Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gly Asp Met Val Asp Leu
      50                      55                      60

Pro Arg Pro Ser Cys Val Thr Leu Gly Val Pro Leu Phe Ser His Leu
      65                      70                      75                      80

Gln Asp Glu Gln Trp Val Asp Tyr Asn Leu Lys Trp Asn Pro Asp Asp
      85                      90                      95

Tyr Gly Gly Val Lys Lys Ile His Ile Pro Ser Glu Lys Ile Trp Arg
      100                     105                     110

Pro Asp Leu Val Leu Tyr Asn Asn Ala Asp Gly Asp Phe Ala Ile Val
      115                     120                     125

Lys Phe Thr Lys Val Leu Leu Gln Tyr Thr Gly His Ile Thr Trp Thr
      130                     135                     140

Pro Pro Ala Ile Phe Lys Ser Tyr Cys Glu Ile Ile Val Thr His Phe
      145                     150                     155                     160

Pro Phe Asp Glu Gln Asn Cys Ser Met Lys Leu Gly Thr Trp Thr Tyr
      165                     170                     175

Asp Gly Ser Val Val Ala Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu
      180                     185                     190

Ser Asn Phe Met Glu Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly
      195                     200                     205

Trp Lys His Ser Val Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu
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Asp Ile Thr Tyr His Phe
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23

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24